AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Currently amended) A method for the fermentative production of ~~at least one sulfur-containing fine chemical~~ L-methionine, which comprises the following steps:

a) fermenting in a medium cells of a coryneform ~~bacteria culture~~ bacterium for producing ~~the at least one sulfur-containing fine chemical~~ L-methionine, ~~wherein~~ the coryneform bacteria ~~express~~ expressing at least one heterologous nucleotide sequence which codes for a protein with O-acetylhomoserine sulfhydrolase (metY) activity, wherein the heterologous nucleotide sequence comprises a nucleotide sequence encoding a metY protein having an amino acid sequence as set forth in SEQ ID NO: 4 or comprises a nucleotide sequence encoding a metY protein having an amino acid sequence with 95% homology or more to the sequence as set forth in SEQ ID NO: 4;

b) concentrating ~~the sulfur-containing fine chemical~~ L-methionine in the medium or in the bacterial cells, and

c) isolating ~~the sulfur-containing fine chemical~~ L-methionine.

2-4. (Cancelled).

5. (Currently amended) The method as claimed in claim 1, wherein the metY-encoding nucleotide sequence comprises a coding sequence ~~according to~~ as set forth in SEQ ID [[NO:1,]] NO: 3~~, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51 and 53 or a nucleotide sequence homologous thereto which codes for a protein with metY activity~~.

6. (Currently amended) The method as claimed in claim 1, wherein the metY-encoding sequence codes for a protein with metY activity, ~~said~~ the protein comprising an amino acid sequence ~~according to~~ as set forth in SEQ ID [[NO:2,]] NO: 4~~, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52 and 54 or an amino acid sequence homologous thereto which represents a protein with metY activity~~.

7. (Previously presented) The method as claimed in claim 1, wherein the coding metY sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

8. (Previously presented) The method as claimed in claim 7, wherein the bacteria is

a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metY sequence under the control of regulatory sequences is used, or

b) a strain in which the coding metY sequence has been integrated into the bacteria chromosome is used.

9. (Previously presented) The method as claimed in claim 1, wherein the coding metY sequence is overexpressed.

10. (Currently amended) The method as claimed in claim 1, wherein the bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of ~~the sulfur-containing fine chemical~~ L-methionine has been ~~amplified or mutated such that its activity is not influenced by metabolic metabolites~~ overexpressed.

11. (Cancelled).

12. (Previously presented) The method as claimed in claim 1, wherein the coryneform bacteria are fermented in which, at the same time, at least one of the genes selected from among

a) the gene lysC, which encodes an aspartate kinase,

b) the glyceraldehyde-3-phosphate dehydrogenase-encoding gene gap,

c) the 3-phosphoglycerate kinase-encoding gene pgk,

d) the pyruvate carboxylase-encoding gene pyc,

e) the triose phosphate isomerase-encoding gene tpi,

f) the homoserine O-acetyltransferase-encoding gene metA,

g) the cystathionine gamma-synthase-encoding gene metB,

h) the cystathionine gamma-lyase-encoding gene metC,

i) serine hydroxymethyltransferase-encoding gene glyA,

j) the methylene tetrahydrofolate reductase-encoding gene metF,

k) the vitamin B12-dependent methionine synthase-encoding gene metH,

l) the phophoserine aminotransferase-encoding gene serC,

m) the phosphoserine phosphatase-encoding gene serB,

n) the serine acetyltransferase-encoding gene cysE, and

o) the gene hom, which encodes a homoserine dehydrogenase,

is overexpressed or mutated in such a way that the activity of the corresponding proteins is influenced by metabolic metabolites to a smaller extent, if at all, compared to nonmutated proteins.

13. (Previously presented) The method as claimed in claim 1, wherein the coryneform bacteria are fermented in which, at the same time, at least one of the genes selected from among

a) the homoserine kinase-encoding gene thrB,

b) the threonine dehydratase-encoding gene ilvA,

c) the threonine synthase-encoding gene thrC,

d) the meso-diaminopimelate D-dehydrogenase-encoding gene ddh,

e) the phosphoenolpyruvate carboxykinase-encoding gene pck,

f) the glucose-6-phosphate 6-isomerase-encoding gene pgi,

g) the pyruvate oxidase-encoding gene poxB,

h) the dihydrodipicolinate synthase-encoding gene dapA,

i) the dihydrodipicolinate reductase-encoding gene dapB; and

j) the diaminopicolinate decarboxylase-encoding gene,

is attenuated by changing the rate of expression or by introducing a specific mutation.

14. (Currently amended) The method as claimed in claim 1, wherein ~~a microorganism~~ the coryneform bacterium is of the species ~~Corynebacterium glutamicum is used~~ *Corynebacterium glutamicum*.

15. (Withdrawn-Currently amended) A method for producing an L-methionine-containing animal feed additive from fermentation broths, which comprises the following steps:

a) culturing and fermenting [[an]] L-methionine-producing ~~microorganism~~ cells of a coryneform bacterium in a fermentation medium;

b) removing water from the L-methionine-containing fermentation broth;

c) removing from 0 to 100% by weight of the biomass formed during fermentation; and

d) drying the fermentation broth obtained according to b) and/or c), in order to obtain the animal feed additive in the desired powder or granule form;

wherein the coryneform bacteria express at least one heterologous nucleotide sequence which codes for a protein with O-acetylhomoserine sulfhydrolase (metY) activity, where the heterologous nucleotide sequence comprises a nucleotide sequence encoding a metY protein having an amino acid sequence as set forth in SEQ ID NO: 4 or comprises a nucleotide sequence encoding a metY protein having an amino acid sequence with 95% homology or more to the sequence as set forth in SEQ ID NO: 4.

16. (Cancelled).

17. (New) The method of claim 1, wherein the metY-encoding sequence is derived from *Mycobacterium tuberculosis*.

18. (New) The method of claim 1, wherein the coryneform bacteria are fermented in which, at the same time, a gene lysC derived from a coryneform bacteria, which encodes an aspartate kinase, is overexpressed.

19. (New) The method of claim 18, wherein the lysC gene is derived from *Corynebacterium glutamicum*.

20. (New) A method for the production of L-methionine, which comprises the following steps:

a) fermenting in a medium cells of a coryneform bacterium for producing of L-methionine, the coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with O-acetylhomoserine sulfhydrolase (metY) activity, wherein the heterologous nucleotide sequence comprises a nucleotide sequence having 95% identity or more to the sequence as set forth in SEQ ID NO: 3;

b) concentrating L-methionine in the medium or in the bacterial cells; and

c) isolating L-methionine.

21. (New) The method of claim 20, wherein the coding metY sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

22. (New) The method of claim 20, wherein

a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metY sequence under the control of regulatory sequences is used, or

b) a strain in which the coding metY sequence has been integrated into the bacteria chromosome is used.

23. (New) The method of claim 20, wherein the coding metY sequence is overexpressed.

24. (New) The method of claim 20, wherein the coryneform bacterium is of the species *Corynebacterium glutamicum*.

25. (New) The method of claim 20, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of L-methionine is overexpressed.

26. (New) The method of claim 25, wherein the at least one further gene is a gene lysC derived from a coryneform bacteria, which encodes an aspartate kinase.